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FULBRIGHT & JAWORSKI L.L.P.

By

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TECH CENTER 1600/2900

LUD 5615 (09905230)

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P#13

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : JAGER, et al.

Serial No : 09/451,739

Filed : November 30, 1999

For : ISOLATED NUCLEIC ACID MOLECULES ENCODING  
CANCER ASSOCIATED ANTIGENS, THE ANTIGENS  
PER SE, AND USES THEREOF

Group Art Unit : 1642

Examiner : G. Nickol

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February 2, 2001

Hon. Commissioner of Patents  
and Trademarks  
Washington, D.C. 20231

**LETTER**

In response to the office action of January 28, please replace the paper copy of the sequence listing and CRF of same with the attached.

The undersigned hereby declares that to the best of his knowledge, the information presented on the attached paper copy of sequence listing and computer readable form thereof are identical to each other and to information set forth in the above referenced patent application as filed. No new matter is believed presented.

Respectfully submitted,

FULBRIGHT & JAWORSKI L.L.P.

By

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Reg. No. 30,946

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New York, New York 10103  
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<110> Jager, Dirk  
Scanlan, Matthew  
Gure, Ali  
Jager, Elke  
Knuth, Alexander  
Old, Lloyd  
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,  
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

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 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp  
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 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu  
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 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu  
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 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr  
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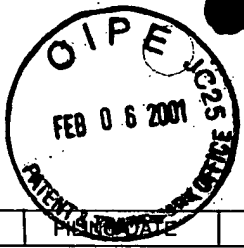
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 Pro Arg Pro Ala Gly Pro Ala Arg Arg Gln Phe Gln Ala Ala Ser Leu  
                     35                      40                      45  
 Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys  
                     50                      55                      60  
 Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala  
 65                      70                      75                      80  
 Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser  
                     85                      90                      95  
 Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu  
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 Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn  
                     165                      170                      175  
 Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys

180					185					190				
Glu	Lys	Lys	Ala	Lys	Thr	Ser	Lys	Lys	Lys	Arg	Ser	Lys	Ala	Lys
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Ala	Glu	Arg	Glu	Ala	Ser	Pro	Ala	Asp	Leu	Pro	Ile	Asp	Pro	Asn
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Pro	Thr	Tyr	Cys	Leu	Cys	Asn	Gln	Val	Ser	Tyr	Gly	Glu	Met	Ile
225					230					235				
Cys	Asp	Asn	Asp	Glu	Cys	Pro	Ile	Glu	Trp	Phe	His	Phe	Ser	Cys
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275					280					285				
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290					294									



UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office

Address: COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
-----------------	-------------	----------------------	---------------------

09/451,739

11/30/95

JAGER

UD-5615

024972

HW/2/0130

FULBRIGHT & JAWORSKI, LLP

666 FIFTH AVE

NEW YORK NY 10103-3198

EXAMINER

NICKOLLS

ART UNIT

PAPER NUMBER

1642

DATE MAILED:

01/30/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

FULBRIGHT & JAWORSKI, LLP

NEW YORK DOCKETING

Docketed ☒ Not Required ☐

Previously ☐ Updated ☐

Docket No: LUD 5615 / NDH

Action: Sequence listing

Reminder: 2/21/2001

Date: Due/Done 2/28/2001

Initials: [Signature]

DOCKET DEPT.  
RECEIVED

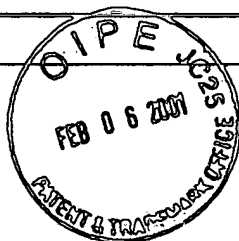
01 FEB - 1 PM 10:09

SEARCH & SERIALIZED

UNITED STATES DEPARTMENT OF COMMERCE  
Patent and Trademark Office  
COMMISSIONER OF PATENTS AND TRADEMARKS  
Washington, D.C. 20231

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/451739			



EXAMINER	
Gary B. Nickol Ph.D.	
ART UNIT	PAPER NUMBER
1642	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application  
Commissioner of Patents

The communication filed on 01/02/01 is not fully responsive for the reasons set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.136 (g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gary Nickol, Ph.D. whose telephone number is (703) 305-7143. The examiner can normally be reached on Monday through Friday from 830am to 630pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. The fax phone number for this Group is (703) 305-3014 or (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

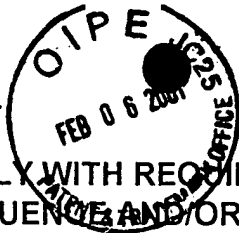
Gary B. Nickol Ph.D.  
January 26, 2001

*G. Nickol*  
ANTHONY C. CAPUTA  
PATENT EXAMINER  
TECHNICAL CENTER 1600/2000

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Application No.: 09/451739

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

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**FEB 13 2001**

**Applicant Must Provide:**

**TECH CENTER 1600/2900**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support

Technical Assistance.....703-287-0200

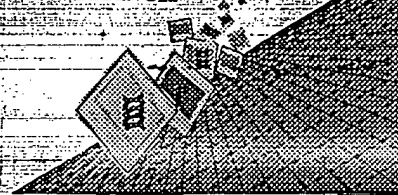
To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

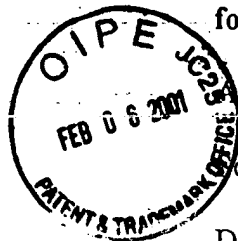
*Nickel*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:



Application Serial Number:

09/451,739B

Source:

1642

Date Processed by STIC:

1/2/2001

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FEB 13 2001

TECH CENTER 1600/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/451,739B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s) \_\_\_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s) \_\_\_\_\_ are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s) \_\_\_\_\_ are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.



2. Nickol



1642

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001

TIME: 11:02:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022001\I451739B.raw

Does Not Comply  
Corrected Diskette Needed

see item 5 on  
Encl  
Summary  
Sheet

1 <110> APPLICANT: Jager, Dirk  
2 Seanlan, Matthew  
3 Gure, Ali  
4 Jager, Elke  
5 Knuth, Alexander  
6 Old, Lloyd  
7 Chen, Yao-tseng  
8 <120> TITLE OF INVENTION: Isolated Nucleic Acid Polynucleotides Encoding Cancer Associated  
9 Antigens.  
10  
11 The Antigens per se, and Uses Thereof  
12  
13 <130> TITLE REFERENCE: LUD 5615  
14  
15 <140> CURRENT APPLICATION NUMBER: 09/451,739B  
16  
17 <141> CURRENT FILING DATE: 1999-11-30  
18  
19 <150> NUMBER OF SEQ ID NOS: 19

ERRORED SEQUENCES

520 <210> SEQ ID NO: 16  
521 <211> LENGTH: 513  
522 <212> TYPE: PRT  
523 <213> ORGANISM: Homo sapiens  
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528 20 25 30  
529 Ile Glu Met Glu Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn  
530 35 40 45  
531 Glu Glu Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Glu  
532 50 55 60  
533 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr  
534 65 70 75 80  
535 Val Ser Glu Lys Asp Val Cys Leu Pro Lys Ala Thr His Glu Lys Glu  
536 85 90 95  
537 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly  
538 100 105 110  
539 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala  
540 115 120 125  
541 Leu Glu Leu Met Asp Met Glu Thr Phe Lys Ala Glu Pro Pro Glu Lys  
542 130 135 140  
543 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Glu Lys Ser Val Pro Asn  
544 145 150 155 160  
545 Lys Ala Leu Glu Leu Lys Asn Glu Glu Thr Leu Arg Ala Asp Glu Met  
546 165 170 175  
547 Phe Pro Ser Glu Ser Lys Glu Lys Lys Val Glu Glu Asn Ser Trp Asp  
548 180 185 190

512 shown (next page)

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001

TIME: 11:02:39

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Output Set: N:\CRF3\01022001\I451739B.raw

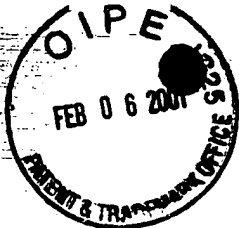
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566      210      215      220
568 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
569 225      230      235      240
571 Arg Ala Arg Glu Leu Glu Lys Asp His Cys Glu Glu Arg Thr Gly Lys
E--> 572      245      250      255
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E--> 575      260      265      270
577 Glu Ala Lys Glu Ile Lys Ser Glu Leu Glu Asn Glu Lys Val Lys Trp
E--> 578      275      280      285
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E--> 581 290      295      300      305
583 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
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E--> 590      340      345      350
592 Ser Asn Leu Asn Glu Val Ser His Thr His Glu Asn Glu Asn Lys Leu
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595 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 596 370      375      380      385
598 Glu Ile Ala Thr Leu Lys His Glu Tyr Glu Glu Lys Glu Asn Lys Tyr
E--> 599      390      395      400
601 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Glu Met
E--> 602      405      410      415
604 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Glu Tyr
E--> 605      420      425      430
607 Ser Gly Glu Leu Lys Val Leu Ile Ala Thr Asn Thr Met Leu Thr Ser
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617 Val Thr Ser Arg Lys Ser Glu Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 618      485      490      495
620 Ala Cys Leu Glu Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 621      500      505      510

```

*misaligned amino  
acid numbers  
(see item 4 on  
Error Summary  
sheet)*

*see next page for more errors*



09/451,739B 3

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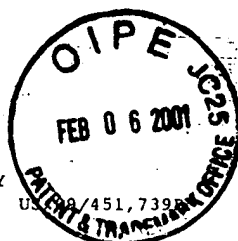
→ see  
item 10  
on Enrol  
Summary Sheet

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tttagaaact acaaatatag gtttgattca aca 1533

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



## VERIFICATION SUMMARY

PATENT APPLICATION: US 2001/01022001

DATE: 01/02/2001

TIME: 11:02:40

Input Set : A:\ES.txt

Output Set: N:\CRF3\01022001\I451739B.raw

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L:26 M:283 W: Missing Blank Line separator, <220> field identifier  
L:29 M:283 W: Missing Blank Line separator, <400> field identifier  
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:1  
L:36 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID:1  
L:87 M:283 W: Missing Blank Line separator, <400> field identifier  
L:133 M:283 W: Missing Blank Line separator, <220> field identifier  
L:134 M:283 W: Missing Blank Line separator, <400> field identifier  
L:167 M:283 W: Missing Blank Line separator, <400> field identifier  
L:203 M:283 W: Missing Blank Line separator, <400> field identifier  
L:264 M:283 W: Missing Blank Line separator, <220> field identifier  
L:265 M:283 W: Missing Blank Line separator, <400> field identifier  
L:314 M:283 W: Missing Blank Line separator, <400> field identifier  
L:367 M:283 W: Missing Blank Line separator, <400> field identifier  
L:390 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:8  
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:8  
L:390 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID:8  
L:399 M:283 W: Missing Blank Line separator, <400> field identifier  
L:407 M:283 W: Missing Blank Line separator, <400> field identifier  
L:415 M:283 W: Missing Blank Line separator, <400> field identifier  
L:422 M:283 W: Missing Blank Line separator, <400> field identifier  
L:431 M:283 W: Missing Blank Line separator, <400> field identifier  
L:439 M:283 W: Missing Blank Line separator, <400> field identifier  
L:450 M:283 W: Missing Blank Line separator, <400> field identifier  
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:15  
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:15  
L:505 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID:15  
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:15  
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:15  
M:440 Repeated in SeqNo 16  
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:15  
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:15  
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:15  
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:15  
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID:15  
L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID:15  
L:524 M:283 W: Missing Blank Line separator, <400> field identifier  
L:572 M:342 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
M:342 Repeated in SeqNo 16  
L:621 M:252 E: No. of Seq. differs. L15:LENGTH:Input:513 Found:512 Seq:16  
L:628 M:283 W: Missing Blank Line separator, <400> field identifier  
L:646 M:283 W: Missing Blank Line separator, <400> field identifier  
L:641 M:283 W: Missing Blank Line separator, <400> field identifier